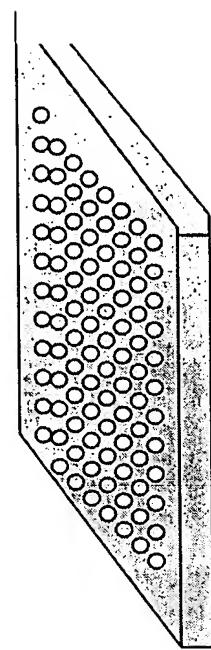
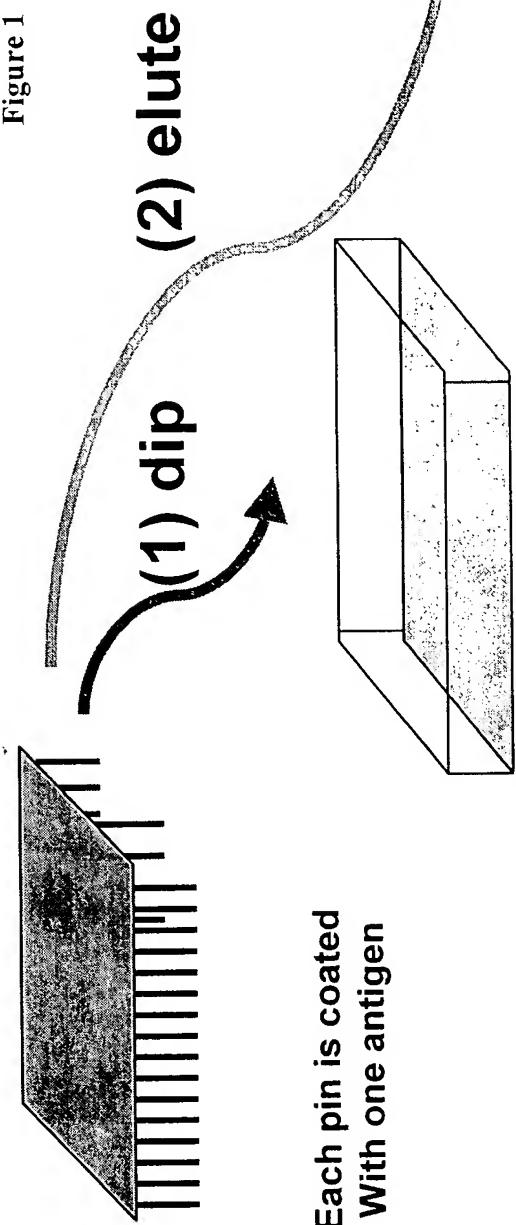


Figure 1



Phage Library of  
Human Antibodies

Elute 96-pin into  
96-well for phage recovery

Figure 2

**“Epitope Scan” over the extracellular domain of a receptor**

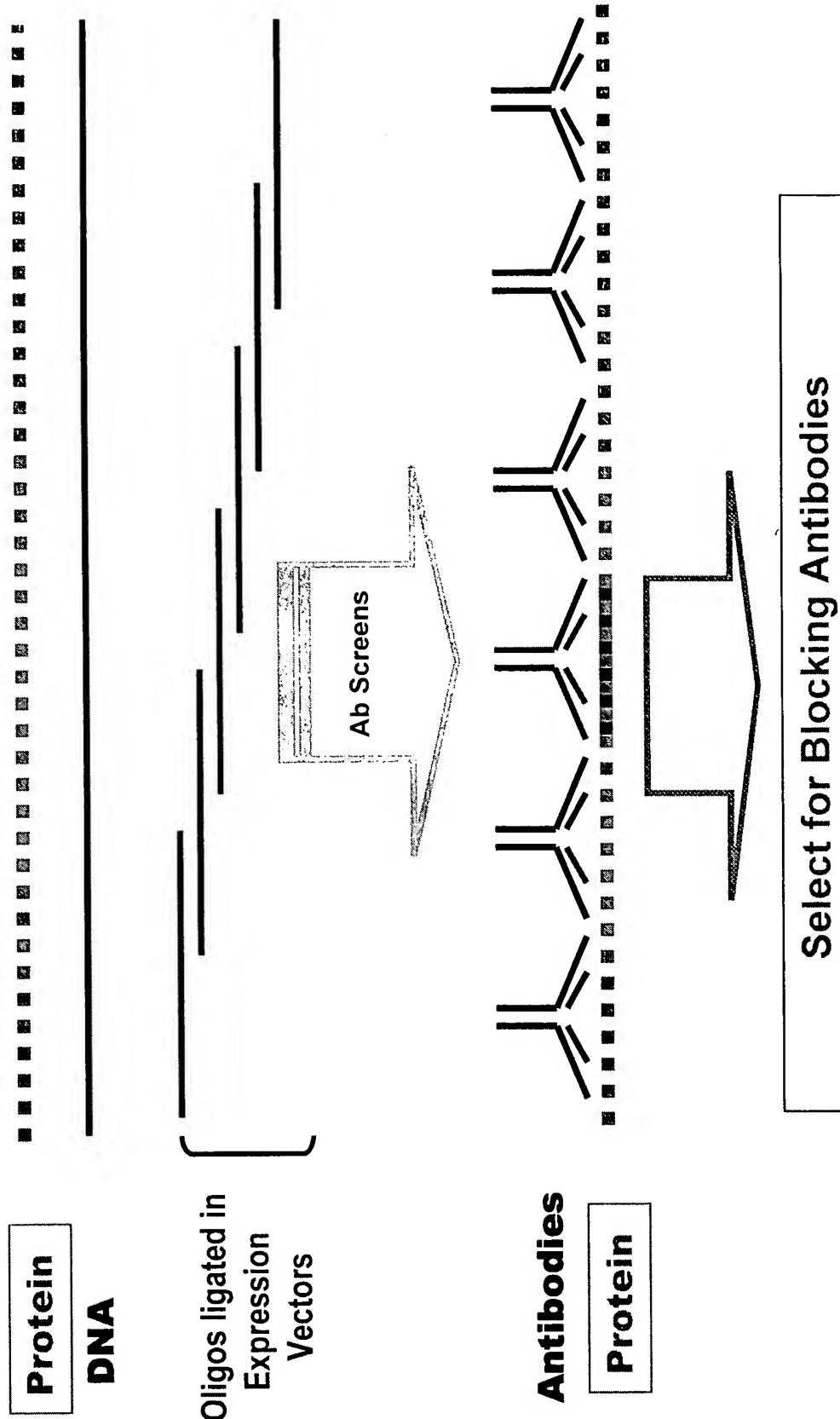
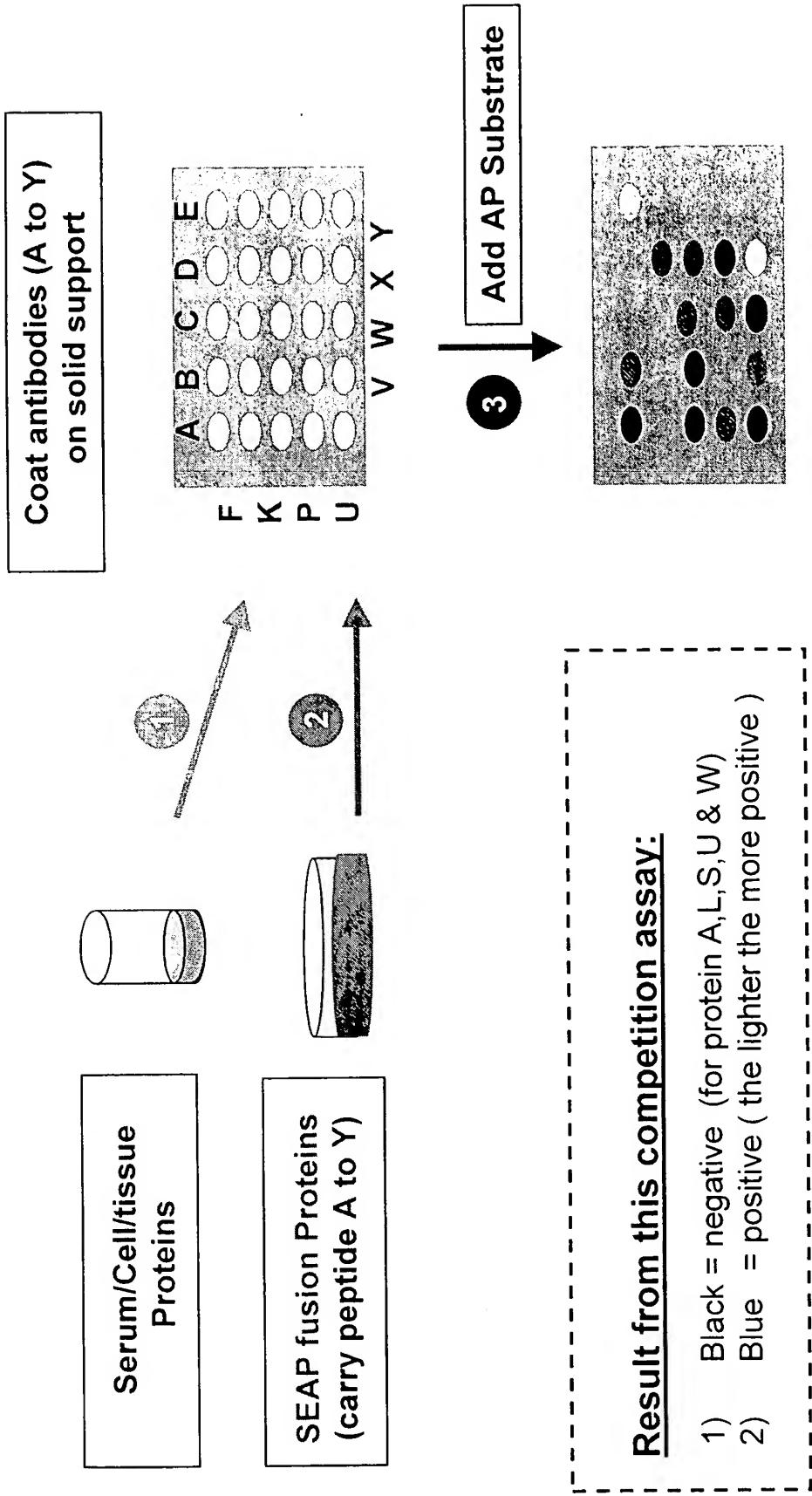


Figure 3



## FIGURE 4

### VEGF ISOFORM ALIGNMENT (VEGF-206, -165, -121)

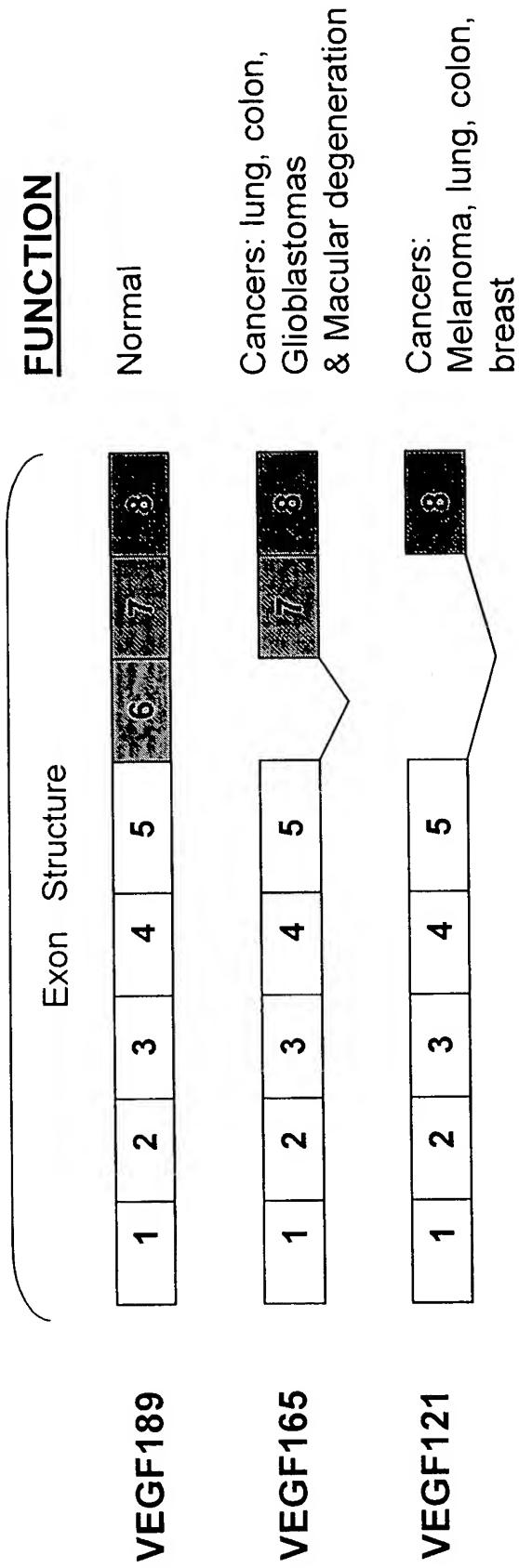
VEGF206 = (232-26)

VEGF165 = (191-26) Missing Exon 6

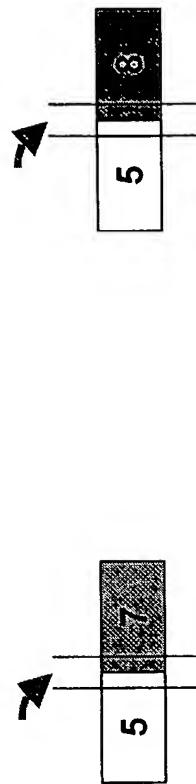
VEGF121 = (147-26) Missing Exon 6 + 7

SIGNAL PEPTIDE 1-26	<u>ISOFORM</u>
MNFLLSWVHW SLALLYLHH AKWSQAAPMA EGGGQNHHEV VKFMDVYQRS YCHPIETLVD	206
MNFLLSWVHW SLALLYLHH AKWSQAAPMA EGGGQNHHEV VKFMDVYQRS YCHPIETLVD	165
MNFLLSWVHW SLALLYLHH AKWSQAAPMA EGGGQNHHEV VKFMDVYQRS YCHPIETLVD	121
ANTIBODY A4.6.1 EPITOPE REGION	
IFQEYPDEIE YIFKPSCVPL MRCGGCCNDE GLECVPTees NITMQIMRIK PHQQHIGEM	206
IFQEYPDEIE YIFKPSCVPL MRCGGCSNDE GLECVPTees NITMQIMRIK PHQQHIGEM	165
IFQEYPDEIE YIFKPSCVPL MRCGGCCNDE GLECVPTees NITMQIMRIK PHQQHIGEM	121
SFLQHNKCEC RPKKDRARQE KKSVRGKGKG QKRKRKKSRY KSWSVYVGAR CCLMPWSLPG	206
SFLQHNKCEC RPKKDRARQE	165
SFLQHNKCEC RPKKDRARQE	121
HEPARIN BINDING DOMAIN	
PHPCGPCSER RKHLFVQDPQ TCKCSCKNTD SRCKARQLEL NERTCRCDKP RR	206
NPCGPCSER RKHLFVQDPQ TCKCSCKNTD SRCKARQLEL NERTCRCDKP RR	165
	121

Figure 5



## SPECIFIC EPITOPES FOR VEGF ISOFORMS



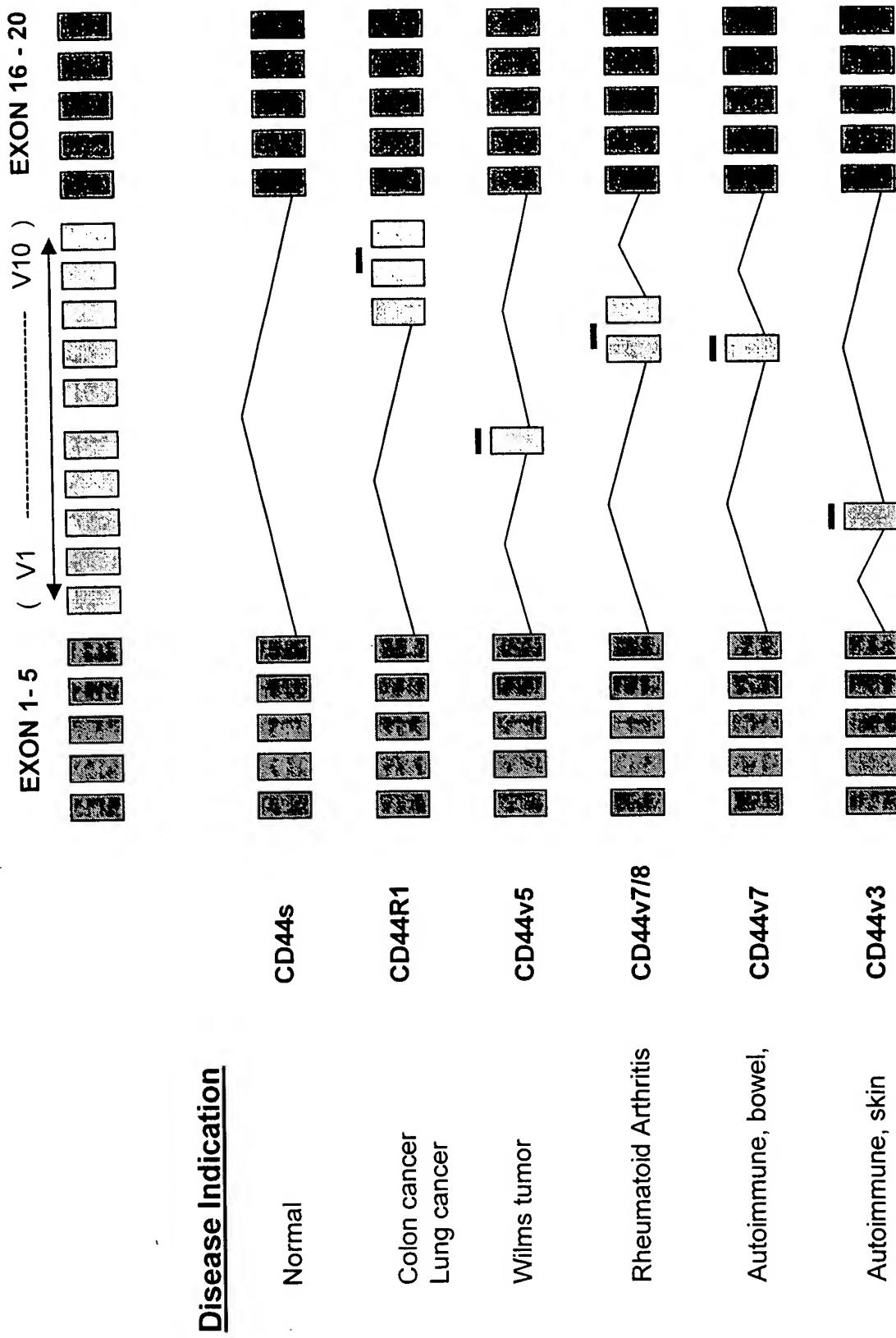
Anti-VEGF121

for melanoma & breast cancer

Anti- VEGF165

for glioblastoma

Figure 6



**Figure 7A**

tcgcggaggc ttggggcagc cggttagctc ggaggtcggt ggcgtgggg ctagcaccag 60  
 cgctctgtcg ggaggcgcag cggttaggtg gaccggtcag cggactcacc ggccaggcg 120  
 ctcggtgctg gaatttgcata ttcattgatc cgggtttat cccttttctt ttttcttaaa 180  
 cattttttt taaaactgta ttgtttctcg tttaattta ttttgcttg ccattcccc 240  
 cttgaatcg gcccacggct tggggagatt gctctacttc cccaaatcac tgtggatttt 300  
 gaaaaaccagc agaaagagga aagaggtac aagagctcca gagagaagtc gaggaagaga 360  
 gagacggggt cagagagagc gcgcggcgt gcgagcagcg aaagcgacag gggcaaagt 420  
 agtgcacctgc ttttgggggt gaccggcga gcgcggcgt agccctcccc cttggatcc 480  
 cgcagctgac cagtcgcgt gacggacaga cagacagaca ccgcggccag cccagctac 540  
 cacctcctcc cccggccggcg gcggacagtgc gacgcggcgg cgagccgcgg gcaggggcg 600  
 gagccgcgc cccggaggcg ggtggagggg gtcggggctc gcggcgtcgc actgaaactt 660  
 ttctgtccaaac ttctgggctg ttctcgcttc ggaggagccg tggccgcgc gggggaaagcc 720  
 gagccgagcg gagccgcgag aagtgcgtac tcggggccggg aggagccgca gccggaggag 780  
 ggggaggagg aagaagagaa ggaagaggag agggggccgc agtggcgtact cggcgtcgg 840  
 aagccggct catggacggg tgaggcggcg gtgtgcgcag acagtgcctcc agccgcgcgc 900  
 gctccccagg ccctggcccg ggcctcggc cggggaggaa gagtagctcg ccgaggcgcc 960  
 gaggagagcg gcccggccca cagcccgagc cggagaggaa gcgcgagccg cccggcccc 1020  
 ggtcgccctt ccgaaacc atg aac ttt ctg ctg tct tgg gtg cat tgg agc 1071  
 Met Asn Phe Leu Leu Ser Trp Val His Trp Ser  
 1 5 10  
  
 ctt gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca 1119  
 Leu Ala Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala  
 15 20 25  
  
 ccc atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg aag ttc 1167  
 Pro Met Ala Glu Gly Gly Gln Asn His His Glu Val Val Lys Phe  
 30 35 40  
  
 atg gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg 1215  
 Met Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val  
 45 50 55  
  
 gac atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca 1263  
 Asp Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro  
 60 65 70 75

**Figure 7B**

tcc tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly 80 85 90	1311
ctg gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg Leu Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met 95 100 105	1359
cg <sup>g</sup> atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta Arg Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu 110 115 120	1407
cag cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa Gln His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln 125 130 135	1455
gaa aaa aaa tca gtt cga gga aag gga aag ggg caa aaa cga aag cgc Glu Lys Lys Ser Val Arg Gly Lys Gly Lys Gln Lys Arg Lys Arg 140 145 150 155	1503
aag aaa tcc cgg tat aag tcc tgg agc gtt ccc tgt ggg cct tgc tca Lys Lys Ser Arg Tyr Lys Ser Trp Ser Val Pro Cys Gly Pro Cys Ser 160 165 170	1551
gag cgg aga aag cat ttg ttt gta caa gat ccg cag acg tgt aaa tgt Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys 175 180 185	1599
tcc tgc aaa aac aca gac tcg cgt tgc aag gcg agg cag ctt gag tta Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu 190 195 200	1647
aac gaa cgt act tgc aga tgt gac aag ccg agg cgg tga gccgggcagg Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg 205 210 215	1696
aggaaggagc ctccctcagg gtttcgg	1723

**Figure 8A**

aattctcgag	ctcgatcgacc	ggtcgacgag	ctcgagggtc	gacgagctcg	aggcgccg	60												
cccgcccccc	accctcgca	gcaccccgcg	cccccgcccc	tcccagccgg	gtccagccgg	120												
agccatgggg	ccggagccgc	agtgagcacc	atg	gag	ctg	gcg	gcc	ttg	tgc	cgc	174							
			Met	Glu	Leu	Ala	Ala	Leu	Cys	Arg								
			1					5										
tgg	ggg	ctc	ctc	gcc	ctc	ttg	ccc	ccc	gga	gcc	gcg	agc	acc	caa	222			
Trp	Gly	Leu	Leu	Leu	Ala	Leu	Leu	Leu	Leu	Pro	Pro	Gly	Ala	Ala	Ser	Thr	Gln	
10						15						20						
gtg	tgc	acc	ggc	aca	gac	atg	aag	ctg	cg	ctc	cct	gcc	agt	ccc	gag	270		
Val	Cys	Thr	Gly	Thr	Asp	Met	Lys	Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu			
25						30			35			40						
acc	cac	ctg	gac	atg	ctc	cgc	cac	ctc	tac	cag	ggc	tgc	cag	gtg	gtg	318		
Thr	His	Leu	Asp	Met	Leu	Arg	His	Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val			
						45			50			55						
cag	gga	aac	ctg	gaa	ctc	acc	tac	ctg	ccc	acc	aat	gcc	agc	ctg	tcc	366		
Gln	Gly	Asn	Leu	Glu	Leu	Thr	Tyr	Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser			
						60			65			70						
ttc	ctg	cag	atc	cag	gag	gtg	cag	ggc	tac	gtg	ctc	atc	gct	cac	414			
Phe	Leu	Gln	Asp	Ile	Gln	Glu	Val	Gln	Gly	Tyr	Val	Leu	Ile	Ala	His			
						75			80			85						
aac	caa	gtg	agg	cag	gtc	cca	ctg	cag	agg	ctg	cg	att	gtg	cga	ggc	462		
Asn	Gln	Val	Arg	Gln	Val	Pro	Leu	Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly			
						90			95			100						
acc	cag	ctc	ttt	gag	gac	aac	tat	gcc	ctg	gcc	gtg	cta	gac	aat	gga	510		
Thr	Gln	Leu	Phe	Glu	Asp	Asn	Tyr	Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly			
						105			110			115			120			
gac	ccg	ctg	aac	aat	acc	acc	cct	gtc	aca	ggg	gcc	tcc	cca	gga	ggc	558		
Asp	Pro	Leu	Asn	Asn	Thr	Thr	Pro	Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly			
						125			130			135						
ctg	cg	gag	ctg	cag	ctt	cga	agc	ctc	aca	gag	atc	ttg	aaa	gga	ggg	606		
Leu	Arg	Glu	Leu	Gln	Leu	Arg	Ser	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly			
						140			145			150						
gtc	ttg	atc	cag	cg	aa	ccc	cag	ctc	tgc	tac	cag	gac	acg	att	ttg	654		
Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln	Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu			
						155			160			165						
tgg	aag	gac	atc	ttc	cac	aag	aac	aac	cag	ctg	gct	ctc	aca	ctg	ata	702		
Trp	Lys	Asp	Ile	Phe	His	Lys	Asn	Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile			
						170			175			180						

Figure 8B

gac acc aac cgc tct cg <sup>g</sup> gcc tgc cac ccc tgt tct ccg atg tgt aag		750	
Asp Thr Asn Arg Ser Arg Ala Cys His Pro Cys Ser Pro Met Cys Lys			
185	190	195	200
ggc tcc cgc tgc tgg gga gag agt tct gag gat tgt cag agc ctg acg		798	
Gly Ser Arg Cys Trp Gly Glu Ser Ser Glu Asp Cys Gln Ser Leu Thr			
205	210	215	
cgc act gtc tgt gcc ggt ggc tgt gcc cgc tgc aag ggg cca ctg ccc		846	
Arg Thr Val Cys Ala Gly Gly Cys Ala Arg Cys Lys Gly Pro Leu Pro			
220	225	230	
act gac tgc tgc cat gag cag tgt gct gcc ggc tgc acg ggc ccc aag		894	
Thr Asp Cys Cys His Glu Gln Cys Ala Ala Gly Cys Thr Gly Pro Lys			
235	240	245	
cac tct gac tgc ctg gcc tgc ctc cac ttc aac cac agt ggc atc tgt		942	
His Ser Asp Cys Leu Ala Cys Leu His Phe Asn His Ser Gly Ile Cys			
250	255	260	
gag ctg cac tgc cca gcc ctg gtc acc tac aac aca gac acg ttt gag		990	
Glu Leu His Cys Pro Ala Leu Val Thr Tyr Asn Thr Asp Thr Phe Glu			
265	270	275	280
tcc atg ccc aat ccc gag ggc cg <sup>g</sup> tat aca ttc ggc gcc agc tgt gtg		1038	
Ser Met Pro Asn Pro Glu Gly Arg Tyr Thr Phe Gly Ala Ser Cys Val			
285	290	295	
act gcc tgt ccc tac aac tac ctt tct acg gac gtg gga tcc tgc acc		1086	
Thr Ala Cys Pro Tyr Asn Tyr Leu Ser Thr Asp Val Gly Ser Cys Thr			
300	305	310	
ctc gtc tgc ccc ctg cac aac caa gag gtg aca gca gag gat gga aca		1134	
Leu Val Cys Pro Leu His Asn Gln Glu Val Thr Ala Glu Asp Gly Thr			
315	320	325	
cag cgg tgt gag aag tgc agc aag ccc tgt gcc cga gtg tgc tat ggt		1182	
Gln Arg Cys Glu Lys Cys Ser Lys Pro Cys Ala Arg Val Cys Tyr Gly			
330	335	340	
ctg ggc atg gag cac ttg cga gag gtg agg gca gtt acc agt gcc aat		1230	
Leu Gly Met Glu His Leu Arg Glu Val Arg Ala Val Thr Ser Ala Asn			
345	350	355	360
atc cag gag ttt gct ggc tgc aag aag atc ttt ggg agc ctg gca ttt		1278	
Ile Gln Glu Phe Ala Gly Cys Lys Lys Ile Phe Gly Ser Leu Ala Phe			
365	370	375	
ctg ccg gag agc ttt gat ggg gac cca gcc tcc aac act gcc ccg ctc		1326	
Leu Pro Glu Ser Phe Asp Gly Asp Pro Ala Ser Asn Thr Ala Pro Leu			
380	385	390	
cag cca gag cag ctc caa gtg ttt gag act ctg gaa gag atc aca ggt		1374	
Gln Pro Glu Gln Leu Gln Val Phe Glu Thr Leu Glu Glu Ile Thr Gly			
395	400	405	

**Figure 8C**

tac cta tac atc tca gca tgg ccg gac agc ctg cct gac ctc agc gtc Tyr Leu Tyr Ile Ser Ala Trp Pro Asp Ser Leu Pro Asp Leu Ser Val 410 415 420	1422
ttc cag aac ctg caa gta atc cg <sup>g</sup> gga cga att ctg cac aat ggc gcc Phe Gln Asn Leu Gln Val Ile Arg Gly Arg Ile Leu His Asn Gly Ala 425 430 435 440	1470
tac tcg ctg acc ctg caa ggg ctg ggc atc agc tgg ctg ggg ctg cgc Tyr Ser Leu Thr Leu Gln Gly Leu Gly Ile Ser Trp Leu Gly Leu Arg 445 450 455	1518
tca ctg agg gaa ctg ggc agt gga ctg gcc ctc atc cac cat aac acc Ser Leu Arg Glu Leu Gly Ser Gly Leu Ala Leu Ile His His Asn Thr 460 465 470	1566
cac ctc tgc ttc gtg cac acg gtg ccc tgg gac cag ctc ttt cgg aac His Leu Cys Phe Val His Thr Val Pro Trp Asp Gln Leu Phe Arg Asn 475 480 485	1614
ccg cac caa gct ctg ctc cac act gcc aac cgg cca gag gac gag tgt Pro His Gln Ala Leu Leu His Thr Ala Asn Arg Pro Glu Asp Glu Cys 490 495 500	1662
gtg ggc gag ggc ctg gcc tgc cac cag ctg tgc gcc cga ggg cac tgc Val Gly Glu Gly Leu Ala Cys His Gln Leu Cys Ala Arg Gly His Cys 505 510 515 520	1710
tgg ggt cca ggg ccc acc cag tgt gtc aac tgc agc cag ttc ctt cgg Trp Gly Pro Gly Pro Thr Gln Cys Val Asn Cys Ser Gln Phe Leu Arg 525 530 535	1758
ggc cag gag tgc gtg gag gaa tgc cga gta ctg cag ggg ctc ccc agg Gly Gln Glu Cys Val Glu Cys Arg Val Leu Gln Gly Leu Pro Arg 540 545 550	1806
gag tat gtg aat gcc agg cac tgt ttg ccg tgc cac cct gag tgt cag Glu Tyr Val Asn Ala Arg His Cys Leu Pro Cys His Pro Glu Cys Gln 555 560 565	1854
ccc cag aat ggc tca gtg acc tgt ttt gga ccg gag gct gac cag tgt Pro Gln Asn Gly Ser Val Thr Cys Phe Gly Pro Glu Ala Asp Gln Cys 570 575 580	1902
gtg gcc tgt gcc cac tat aag gac cct ccc ttc tgc gtg gcc cgc tgc Val Ala Cys Ala His Tyr Lys Asp Pro Pro Phe Cys Val Ala Arg Cys 585 590 595 600	1950
ccc agc ggt gtg aaa cct gac ctc tcc tac atg ccc atc tgg aag ttt Pro Ser Gly Val Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe 605 610 615	1998

**Figure 8D**

cca gat gag gag ggc gca tgc cag cct tgc ccc atc aac tgc acc cac Pro Asp Glu Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys Thr His 620 625 630	2046
tcc tgt gtg gac ctg gat gac aag ggc tgc ccc gcc gag cag aga gcc Ser Cys Val Asp Leu Asp Asp Lys Gly Cys Pro Ala Glu Gln Arg Ala 635 640 645	2094
agc cct ctg acg tcc atc gtc tct gcg gtg gtt ggc att ctg ctg gtc Ser Pro Leu Thr Ser Ile Val Ser Ala Val Val Gly Ile Leu Leu Val 650 655 660	2142
gtg gtc ttg ggg gtg gtc ttt ggg atc ctc atc aag cga cgg cag cag Val Val Leu Gly Val Val Phe Gly Ile Leu Ile Lys Arg Arg Gln Gln 665 670 675 680	2190
aag atc cgg aag tac acg atg cgg aga ctg ctg cag gaa acg gag ctg Lys Ile Arg Lys Tyr Thr Met Arg Arg Leu Leu Gln Glu Thr Glu Leu 685 690 695	2238
gtg gag ccg ctg aca cct agc gga gcg atg ccc aac cag gcg cag atg Val Glu Pro Leu Thr Pro Ser Gly Ala Met Pro Asn Gln Ala Gln Met 700 705 710	2286
cg <sup>g</sup> atc ctg aaa gag acg gag ctg agg aag gtg aag gtg ctt gga tct Arg Ile Leu Lys Glu Thr Glu Leu Arg Lys Val Lys Val Leu Gly Ser 715 720 725	2334
ggc gct ttt ggc aca gtc tac aag ggc atc tgg atc cct gat ggg gag Gly Ala Phe Gly Thr Val Tyr Lys Gly Ile Trp Ile Pro Asp Gly Glu 730 735 740	2382
aat gtg aaa att cca gtg gcc atc aaa gtg ttg agg gaa aac aca tcc Asn Val Lys Ile Pro Val Ala Ile Lys Val Leu Arg Glu Asn Thr Ser 745 750 755 760	2430
ccc aaa gcc aac aaa gaa atc tta gac gaa gca tac gtg atg gct ggt Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Gly 765 770 775	2478
gtg ggc tcc cca tat gtc tcc cgc ctt ctg ggc atc tgc ctg aca tcc Val Gly Ser Pro Tyr Val Ser Arg Leu Leu Gly Ile Cys Leu Thr Ser 780 785 790	2526
acg gtg cag ctg gtg aca cag ctt atg ccc tat ggc tgc ctc tta gac Thr Val Gln Leu Val Thr Gln Leu Met Pro Tyr Gly Cys Leu Leu Asp 795 800 805	2574
cat gtc cgg gaa aac cgc gga cgc ctg ggc tcc cag gac ctg ctg aac His Val Arg Glu Asn Arg Gly Arg Leu Gly Ser Gln Asp Leu Leu Asn 810 815 820	2622

**Figure 8E**

tgg tgt atg cag att gcc aag ggg atg agc tac ctg gag gat gtg cgg Trp Cys Met Gln Ile Ala Lys Gly Met Ser Tyr Leu Glu Asp Val Arg 825 830 835 840	2670
ctc gta cac agg gac ttg gcc gct cg <sup>g</sup> aac gtg ctg gtc aag agt ccc Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Ser Pro 845 850 855	2718
aac cat gtc aaa att aca gac ttc ggg ctg gct cg <sup>g</sup> ctg gac att Asn His Val Lys Ile Thr Asp Phe Gly Leu Ala Arg Leu Leu Asp Ile 860 865 870	2766
gac gag aca gag tac cat gca gat ggg ggc aag gtg ccc atc aag tgg Asp Glu Thr Glu Tyr His Ala Asp Gly Gly Lys Val Pro Ile Lys Trp 875 880 885	2814
atg gcg ctg gag tcc att ctc cgc cg <sup>g</sup> ttc acc cac cag agt gat Met Ala Leu Glu Ser Ile Leu Arg Arg Arg Phe Thr His Gln Ser Asp 890 895 900	2862
gtg tgg agt tat ggt gtg act gtg tgg gag ctg atg act ttt ggg gcc Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ala 905 910 915 920	2910
aaa cct tac gat ggg atc cca gcc cg <sup>g</sup> gag atc cct gac ctg ctg gaa Lys Pro Tyr Asp Gly Ile Pro Ala Arg Glu Ile Pro Asp Leu Leu Glu 925 930 935	2958
aag ggg gag cg <sup>g</sup> ctg ccc cag ccc atc tgc acc att gat gtc tac Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr 940 945 950	3006
atg atc atg gtc aaa tgt tgg atg att gac tct gaa tgt cg <sup>g</sup> cca aga Met Ile Met Val Lys Cys Trp Met Ile Asp Ser Glu Cys Arg Pro Arg 955 960 965	3054
ttc cg <sup>g</sup> gag ttg gtg tct gaa ttc tcc cgc atg gcc agg gac ccc cag Phe Arg Glu Leu Val Ser Glu Phe Ser Arg Met Ala Arg Asp Pro Gln 970 975 980	3102
cgc ttt gtg gtc atc cag aat gag gac ttg ggc cca gcc agt ccc ttg Arg Phe Val Val Ile Gln Asn Glu Asp Leu Gly Pro Ala Ser Pro Leu 985 990 995 1000	3150
gac agc acc ttc tac cgc tca ctg ctg gag gac gat gac atg ggg Asp Ser Thr Phe Tyr Arg Ser Leu Leu Glu Asp Asp Asp Met Gly 1005 1010 1015	3195
gac ctg gtg gat gct gag gag tat ctg gta ccc cag cag ggc ttc Asp Leu Val Asp Ala Glu Glu Tyr Leu Val Pro Gln Gln Gly Phe 1020 1025 1030	3240

**Figure 8F**

ttc tgt cca gac cct	gcc ccg ggc gct ggg	ggc atg gtc cac cac	3285
Phe Cys Pro Asp Pro	Ala Pro Gly Ala Gly	Gly Met Val His His	
1035	1040	1045	
agg cac cgc agc tca	tct acc agg agt ggc	ggt ggg gac ctg aca	3330
Arg His Arg Ser Ser	Ser Thr Arg Ser Gly	Gly Gly Asp Leu Thr	
1050	1055	1060	
cta ggg ctg gag ccc	tct gaa gag gag gcc	ccc agg tct cca ctg	3375
Leu Gly Leu Glu Pro	Ser Glu Glu Ala	Pro Arg Ser Pro Leu	
1065	1070	1075	
gca ccc tcc gaa ggg	gct ggc tcc gat gta	ttt gat ggt gac ctg	3420
Ala Pro Ser Glu Gly	Ala Gly Ser Asp Val	Phe Asp Gly Asp Leu	
1080	1085	1090	
gga atg ggg gca gcc	aag ggg ctg caa agc	ctc ccc aca cat gac	3465
Gly Met Gly Ala Ala	Lys Gly Leu Gln Ser	Leu Pro Thr His Asp	
1095	1100	1105	
ccc agc cct cta cag	cgg tac agt gag gac	ccc aca gta ccc ctg	3510
Pro Ser Pro Leu Gln	Arg Tyr Ser Glu Asp	Pro Thr Val Pro Leu	
1110	1115	1120	
ccc tct gag act gat	ggc tac gtt gcc ccc	ctg acc tgc agc ccc	3555
Pro Ser Glu Thr Asp	Gly Tyr Val Ala Pro	Leu Thr Cys Ser Pro	
1125	1130	1135	
cag cct gaa tat gtg	aac cag cca gat gtt	cgg ccc cag ccc cct	3600
Gln Pro Glu Tyr Val	Asn Gln Pro Asp Val	Arg Pro Gln Pro Pro	
1140	1145	1150	
tcg ccc cga gag ggc	cct ctg cct gct gcc	cga cct gct ggt gcc	3645
Ser Pro Arg Glu Gly	Pro Leu Pro Ala Ala	Arg Pro Ala Gly Ala	
1155	1160	1165	
act ctg gaa agg gcc	aag act ctc tcc cca	ggg aag aat ggg gtc	3690
Thr Leu Glu Arg Ala	Lys Thr Leu Ser Pro	Gly Lys Asn Gly Val	
1170	1175	1180	
gtc aaa gac gtt ttt	gcc ttt ggg ggt gcc	gtg gag aac ccc gag	3735
Val Lys Asp Val Phe	Ala Phe Gly Gly Ala	Val Glu Asn Pro Glu	
1185	1190	1195	
tac ttg aca ccc cag	gga gga gct gcc cct	cag ccc cac cct cct	3780
Tyr Leu Thr Pro Gln	Gly Gly Ala Ala Pro	Gln Pro His Pro Pro	
1200	1205	1210	
cct gcc ttc agc cca	gcc ttc gac aac ctc	tat tac tgg gac cag	3825
Pro Ala Phe Ser Pro	Ala Phe Asp Asn Leu	Tyr Tyr Trp Asp Gln	
1215	1220	1225	

**Figure 8G**

gac cca cca gag cg <sup>g</sup> ggg gct cca ccc agc acc ttc aaa ggg aca	3870
Asp Pro Pro Glu Arg Gly Ala Pro Pro Ser Thr Phe Lys Gly Thr	
1230 1235 1240	
cct acg gca gag aac cca gag tac ctg ggt ctg gac gtg cca gtg	3915
Pro Thr Ala Glu Asn Pro Glu Tyr Leu Gly Leu Asp Val Pro Val	
1245 1250 1255	
tga accagaaggc caagtccgca gaagccctga tgtgtcctca gggagcaggg	3968
aaggcctgac ttctgctggc atcaagaggt gggagggccc tccgaccact tccaggggaa	4028
cctgccatgc caggaacctg tcctaaggaa cttcccttcc tgcttgagtt cccagatggc	4088
tggaaggggt ccagcctcgt tggaagagga acagcactgg ggagtcttg tggattctga	4148
ggccctgccc aatgagactc tagggtccag tggatgccac agcccagctt ggccctttcc	4208
ttccagatcc tgggtactga aagccttagg gaagctggcc tgagagggga agcggcccta	4268
agggagtgtc taagaacaaa agcgaccat tcagagactg tccctgaaac ctagtactgc	4328
cccccatgag gaaggaacag caatggtgc agtatccagg ctttgtacag agtgccttc	4388
tgttagtt ttactttttt tgttttgttt tttaaagac gaaataaaga cccaggggag	4448
aatgggtgtt gtatggggag gcaagtgtgg ggggtccttc tccacaccca ctttgtccat	4508
ttgcaaataat attttggaaa ac	4530

**Figure 9A**

agcccccaagc ttaccacctg cacccggaga gctgtgtgc acc atg tgg gtc ccg Met Trp Val Pro 1	55
gtt gtc ttc ctc acc ctg tcc gtg acg tgg att ggt gct gca ccc ctc Val Val Phe Leu Thr Leu Ser Val Thr Trp Ile Gly Ala Ala Pro Leu 5 10 15 20	103
atc ctg tct cgg att gtg gga ggc tgg gag tgc gag aag cat tcc caa Ile Leu Ser Arg Ile Val Gly Gly Trp Glu Cys Glu Lys His Ser Gln 25 30 35	151
ccc tgg cag gtg ctt gtg gcc tct cgt ggc agg gca gtc tgc ggc ggt Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala Val Cys Gly Gly 40 45 50	199
gtt ctg gtg cac ccc cag tgg gtc ctc aca gct gcc cac tgc atc agg Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala His Cys Ile Arg 55 60 65	247
aac aaa agc gtg atc ttg ctg ggt cgg cac agc ctg ttt cat cct gaa Asn Lys Ser Val Ile Leu Leu Gly Arg His Ser Leu Phe His Pro Glu 70 75 80	295
gac aca ggc cag gta ttt cag gtc agc cac agc ttc cca cac ccg ctc Asp Thr Gly Gln Val Phe Gln Val Ser His Ser Phe Pro His Pro Leu 85 90 95 100	343
tac gat atg agc ctc ctg aag aat cga ttc ctc agg cca ggt gat gac Tyr Asp Met Ser Leu Leu Lys Asn Arg Phe Leu Arg Pro Gly Asp Asp 105 110 115	391
tcc agc cac gac ctc atg ctg ctc cgc ctg tca gag cct gcc gag ctc Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu Pro Ala Glu Leu 120 125 130	439
acg gat gct gtg aag gtc atg gac ctg ccc acc cag gag cca gca ctg Thr Asp Ala Val Lys Val Met Asp Leu Pro Thr Gln Glu Pro Ala Leu 135 140 145	487
ggg acc acc tgc tac gcc tca ggc tgg ggc agc att gaa cca gag gag Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Glu 150 155 160	535
ttc ttg acc cca aag aaa ctt cag tgt gtg gac ctc cat gtt att tcc Phe Leu Thr Pro Lys Lys Leu Gln Cys Val Asp Leu His Val Ile Ser 165 170 175 180	583
aat gac gtg tgt gcg caa gtt cac cct cag aag gtg acc aag ttc atg Asn Asp Val Cys Ala Gln Val His Pro Gln Lys Val Thr Lys Phe Met 185 190 195	631

**Figure 9B**

ctg tgt gct gga cgc tgg aca ggg ggc aaa agc acc tgc tcg ggt gat Leu Cys Ala Gly Arg Trp Thr Gly Gly Lys Ser Thr Cys Ser Gly Asp 200 205 210	679
tct ggg ggc cca ctt gtc tgt aat ggt gtg ctt caa ggt atc acg tca Ser Gly Gly Pro Leu Val Cys Asn Gly Val Leu Gln Gly Ile Thr Ser 215 220 225	727
tgg ggc agt gaa cca tgt gcc ctg ccc gaa agg cct tcc ctg tac acc Trp Gly Ser Glu Pro Cys Ala Leu Pro Glu Arg Pro Ser Leu Tyr Thr 230 235 240	775
aag gtg gtg cat tac cgg aag tgg atc aag gac acc atc gtg gcc aac Lys Val Val His Tyr Arg Lys Trp Ile Lys Asp Thr Ile Val Ala Asn 245 250 255 260	823
ccc tga gcacccctat caacccctta ttgttagtaaa cttggAACCT tggAAATgac Pro	879
caggccaaga ctcaagcctc cccagttcta ctgaccttg tccttaggtg tgaggtccag ggttgctagg aaaagaaaatc agcagacaca ggtgttagacc agagtgttc ttaaatggtg taattttgtc ctctctgtgt cctggggaat actggccatg cctggagaca tatcactcaa tttctctgag gacacagata ggtgggggtg tctgtgttat ttgtgggta cagagatgaa agaggggtgg gatccacact gagagagtgg agagtgacat gtgctggaca ctgtccatga agcactgagc agaagctgga ggcacaacgc accagacact cacagcaagg atggagctga aaacataacc cactctgtcc tggaggcact gggaagccta gagaaggctg tgagccaagg agggagggtc ttcccttggc atggatgg gatgaagtaa ggagagggac tggacccct ggaagctgat tcactatggg gggaggtgta ttgaagtctt ccagacaacc ctcagattt atgatttcct agtagaactc acagaaataa agagctgtta tactgtg	939 999 1059 1119 1179 1239 1299 1359 1419 1466